

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 30, 2002, 17:23:15 ; Search time 16.39 Seconds

(without alignments)
656.620 Million cell updates/sec

Title: US-09-730-617-4

Perfect score: 568

Sequence: 1 MFGSLHFAALLAGVVPVLSM.....LSRPAPQIQVRRLLVQLLQK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_71:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	386	68.0	117	2 A37178	neuromedin B precu
2	285	50.2	76	2 A28945	neuromedin B precu
3	152	26.8	32	1 B5PGMB	neuromedin B-32 -
4	97.5	17.2	138	2 A26182	gastrin-releasing
5	97.5	17.2	148	1 B26182	gastrin-releasing
6	95.5	16.8	134	2 A47010	gastrin-releasing
7	94	16.5	120	2 A47201	bombesin-like pepti
8	90.5	15.9	147	2 A40922	gastrin-releasing
9	83	14.6	155	2 A42437	gastrin-releasing
10	79.5	14.0	90	2 B57058	Phe-8 phyllolitor
11	77.5	13.6	119	2 A39261	bombesin precursor
12	74.5	13.1	2717	2 A34203	DNA-binding protei
13	74	13.0	260	2 A36949	28.9k basic DNA-bi
14	74	13.0	297	2 F87567	Integral membrane
15	74	13.0	577	2 G82806	DNA primase Xf0430
16	73.5	12.9	90	2 A57058	Lau-8 phyllolitor
17	71.5	12.6	4302	2 A38971	polycyclic kidney
18	70	12.3	107	1 B5TDY	bombesin precursor
19	69.5	12.2	755	2 T20320	hypothetical prote
20	69.5	12.2	1504	2 T49886	glycine/proline-ri
21	69	12.1	145	2 A46703	ribosomal protein
22	69	12.1	394	2 D87327	hypothetical prote
23	68.5	12.1	756	2 F70815	hypothetical prote
24	68.5	12.1	403	2 T49294	hypothetical prote
25	68.5	12.1	726	2 T34638	hypothetical prote
26	68.5	12.1	1400	2 T52359	hypothetical prote
27	67.5	11.9	709	2 C28821	1-phosphatidylinos
28	67	11.8	186	2 D83515	hypothetical prote
29	67	11.8	441	2 S76513	hypothetical prote

30	67	11.8	497	2 C75618	hypothetical prote
31	67	11.8	698	2 A90528	hypothetical prote
32	67	11.8	15281	2 S41309	cyclosporin synthe
33	66.5	11.7	347	2 E75251	probable cytochrom
34	66.5	11.7	396	1 H70730	cytochrome P450 Rv
35	66.5	11.7	745	1 PC4183	1-phosphatidylinos
36	66.5	11.7	756	1 B28821	1-phosphatidylinos
37	66	11.6	82	2 B28945	ranastatin precurs
38	66	11.6	158	2 D72714	hypothetical prote
39	66	11.6	584	2 D84264	hypothetical prote
40	66	11.6	996	2 A71080	hypothetical prote
41	66	11.6	1539	2 G70630	probable ctpH prot
42	66	11.6	2493	2 S72349	nonstructural poly
43	65.5	11.5	272	2 C87479	acylttransferase fa
44	65.5	11.5	1265	1 A37967	neural cell adhesi
45	65	11.4	155	2 I64057	bacteriostatin c

ALIGNMENTS

RESULT 1
A37178
neuromedin B precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 12-Apr-1995
C:Accession: A37178
R:Wada, E.; Way, J.; Lebacqz-Verheyden, A.M.; Battey, J.F.
J. Neurosci. 10, 2917-2930, 1990
A:Title: Neuromedin B and gastrin-releasing peptide mRNAs are differentially distribu
A:Reference number: A37178; MUID:90376141
A:Accession: A37178
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-117 <WAD>
C:Superfamily: gastrin-releasing peptide

Query Match 68.0%; Score 386; DB 2; Length 117;

Best Local Similarity 75.5%; Pred. No. 6.5e-34;

Matches 77; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 5 LILFALLAGVVPVLSMDPEPRSRASKIRVHSRGKLTATGHPMGKSLSPSSPPLGAP 64
DB 14 LILFALFVSGIRPFSDLPPEPRSRASKIRVHRGMLMTGHPMGKSLSPSSLVGTAP 73
QY 65 HTSLRDQRLQSLHDLGLILKALGVSLSRPAPQIQVRRLL 106
DB 74 PTTREORQLSLHDLRLILLQKALGMNLGAPPIQVRRLL 115

RESULT 2
A28945
neuromedin B precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 12-Apr-1995
C:Accession: A28945
R:Kriane, I.M.; Naylor, S.L.; Helin-Davis, D.; Chin, W.W.; Spindel, E.R.
J. Biol. Chem. 263, 13317-13323, 1988
A:Title: Molecular cloning of cDNAs encoding the human bombesin-like peptide neuromed
A:Reference number: A92667; MUID:88330837
A:Accession: A28945
A:Molecule type: mRNA
A:Residues: 1-76 <KRA>
C:Superfamily: gastrin-releasing peptide

Query Match 50.2%; Score 285; DB 2; Length 76;

Best Local Similarity 87.5%; Pred. No. 2.1e-23;

Matches 56; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 MFGSLHFAALLAGVVPVLSMDPEPRSRASKIRVHSRGKLTATGHPMGKSLSPSSPPL 60
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Db      10  MEGSLLEFALLAAGVAPLSMDLPEPRSRASKIRVHSGCNLWATGHFMGKKSLEPSPSHW  69
Oy      61  GTAP  64
Db      70  GLP  73

RESULT  3
BSPGMB
neuromedin B-32 - pig
N:Contains: neuromedin B
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-Feb-1984 #sequence_revision 31-Dec-1992 #text_change 20-Mar-1998
A:Accession: B60301; A01565; A60301
R:Minamino, N.; Kangawa, K.; Matsuo, H.
Regul. Pept. 19, 127, 1987
A:Title: Neuromedin B and neuromedin C: two mammalian bombesin-like peptides identified
A:Reference number: A60301
A:Accession: B60301
A:Molecule type: protein
A:Residues: 1-32 <MIN>
A:Note: this reference is an abstract
R:Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 114, 541-548, 1993
A:Title: Neuromedin B: a novel bombesin-like peptide identified in porcine spinal cord.
A:Reference number: A01565; MUID:83282813
A:Accession: A01565
A:Molecule type: protein
A:Residues: 23-32 <M12>
A:Note: the structure of the peptide was confirmed by synthesis
C:Comment: The biological source of neuromedin B is spinal cord. It stimulates smooth m
C:Superfamily: gastrin-releasing peptide
C:Keywords: amidated carboxyl end; hormone; neuropeptide; spinal cord
F:1-32/Product: neuromedin B-32 #status experimental <B32>
F:23-32/Product: neuromedin B #status experimental <NMB>
F:32/Modified site: amidated carboxyl end (Met) #status experimental

Query Match      26.8%; Score 152; DB 1; Length 32;
Best Local Similarity 87.1%; Pred. No. 1,16-09;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      17  PLSMDLPEPRSRASKIRVHSGCNLWATGHFM  47
Db      2  PLSMDLPEPRSRASKIRVHSGCNLWATGHFM  32

RESULT  4
A26182
gastrin-releasing peptide precursor splice form III - human
N:Alternate names: gastrin-releasing peptide form I
C:Species: Homo sapiens (man)
C:Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Feb-2000
A:Accession: A26182; B32032; C46576
R:Spindel, E.R.; Zilberberg, M.D.; Habener, J.F.; Chlin, W.W.
Proc. Natl. Acad. Sci. U.S.A. 83, 19-23, 1986
A:Title: Two prohormones for gastrin-releasing peptide are encoded by two mRNAs differentia
A:Reference number: A94091; MUID:86094341
A:Accession: A26182
A:Molecule type: mRNA
A:Residues: 1-138 <SP1>
R:Reeve Jr., J.R.; Cutcliffe, F.; Vigna, S.R.; Heubner, V.; Lee, T.D.; Shively, J.E.; Ho
J. Biol. Chem. 263, 1928-1932, 1988
A:Title: Multiple gastrin-releasing peptide gene-associated peptides are produced by a
A:Reference number: A32032
A:Accession: B32032
A:Molecule type: protein
A:Residues: 125-135 <REE>
R:Sanaville, E.A.; Lebacqz-Verheyden, A.M.; Spindel, E.R.; Cutcliffe, F.; Gazdar, A.F.; Ba
J. Biol. Chem. 261, 2451-2457, 1986
A:Title: Expression of the gastrin-releasing peptide gene in human small cell lung cancer
A:Accession: C46576

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A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 119-138 <SAU>
A:Cross-references: GB:M12512; NID:g183637; PIDN:AAA52610.1; PID:g386755
C:Comment: The nomenclature for the precursor splice forms I, II, and III is taken from Genetics:
A:Gene: GDB:GRP
A:Cross-references: GDB:119284; OMIM:137260
A:Map position: 18q21.32-18q21.33
C:Superfamily: gastrin-releasing peptide
C:Keywords: alternative splicing; amidated carboxyl end; neuropeptide
F:1-23/Domin: signal sequence #status predicted <Sig>
F:24-50/Product: gastrin-releasing peptide #status experimental <MAT1>
F:51-50/Product: neuromedin C #status experimental <MAT2>
F:50/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 17.28; Score 97.5; DB 2; Length 138;
Best Local Similarity 34.5%; Pred. No. 0.0039;
Matches 40; Conservative 13; Mismatches 26; Indels 37; Gaps 7;

OY 1 MEGSLPALLAGVPLPSMDLPEPRSRASKI-----RVHSRGLMIGHFGMKKS 51
Db 1 MRGSLPLVLAL-VLCIA-----PRGNAYLPACGGCVLTAKMPRGNNHNAVGLMGKKS 54
OY 52 L-EPPSPSLPGTAPHTSLRDQRL-----QLSHDLGLTLKK-----KALG 90
Db 55 TGESSSVSEHG-----SLKOOLREYIRWEFAARNILGLEAKENRNHQPOPKALG 105

RESULT 5
B26182
gastrin-releasing peptide precursor splice form I [validated] - human
N:Contains: gastrin-releasing peptide precursor splice form II; neuromedin C
C:Species: Homo sapiens (man)
C:Date: 18-Feb-2000 #sequence revision 18-Feb-2000 #text change 08-Dec-2000
C:Accession: B26182; A40913; A46576; B46576; B60784; C60784; A30327; 152705; A31200
R:Spindel, E.R.; Zilberberg, M.D.; Habener, J.F.; Chin, W.W.
A>Title: Two prohormones for gastrin-releasing peptide are encoded by two mRNAs differing by one amino acid
A:Reference number: A94091; MUID:86094341
A:Accession: B26182
A:Molecule type: mRNA
A:Residues: 1-148 <SPI1>
A:Cross-references: GB:K02054; NID:g183642; PIDN:AAA52613.1; PID:g306807
R:Spindel, E.R.; Zilberberg, M.D.; Chin, W.W.
Mol. Endocrinol. 1, 224-232, 1987
A>Title: Analysis of the gene and multiple messenger ribonucleic acids (mRNAs) encoding gastrin-releasing peptide precursor splice forms I and II
A:Reference number: A40913; MUID:88288196
A:Accession: A40913
A:Molecule type: DNA
A:Residues: 1-3, 'R', 5-148 <SPI2>
R:Sausville, E.A.; Lebacqz-Verheyden, A.M.; Spindel, E.R.; Cuttitta, F.; Gazdar, A.F.; et al.
Biochem. Biophys. Res. Commun. 261, 2451-2457, 1986
A>Title: Expression of the gastrin-releasing peptide gene in human small cell lung carcinoma
A:Reference number: A46576; MUID:86111953
A:Accession: A46576
A:Molecule type: mRNA
A:Residues: 119-148 <SAU1>
A:Cross-references: GB:M12512; NID:g183637; PIDN:AAA52611.1; PID:g386756
A:Experimental source: splice form I
A:Accession: B46576
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 119-127, 135-148 <SAU2>
A:Cross-references: GB:M12512; NID:g183637; PIDN:AAA52612.1; PID:g386757
A:Experimental source: splice form II
R:Conlon, J.M.; McGregor, G.P.; Wallin, G.; Grimelius, L.; Thim, L.
Cancer Res. 48, 2412-2416, 1988
A>Title: Molecular forms of calcitonin receptor-related peptide and gastrin-releasing peptide in human small intestine
A:Reference number: A60784; MUID:88184561
A:Accession: B60784
A:Molecule type: protein

A:Residues: 24-45 <CON>
 A:Accession: C60784
 A:Molecule type: protein
 A:Residues: 41-50 <CO2>
 R:Reve Jr., J.R.; Cuttitta, F.; Vigna, S.R.; Heubner, V.; Lee, T.D.; Shively, J.E.; Ho, J. Biol. Chem. 263, 1928-1932, 1988
 A:Title: Multiple gastrin-releasing peptide gene-associated peptides are produced by a h
 A:Reference number: A32032
 A:Accession: A32032
 A:Molecule type: protein
 A:Residues: 95-110 <REE>
 R:Nagalla, S.R.; Spindel, E.R.
 Cancer Res. 54, 4461-4467, 1994
 A:Title: Functional analysis of the 5'-flanking region of the human gastrin-releasing pe
 A:Reference number: 152705; MUID:94320083
 A:Accession: 152705
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-3, 'R', '5'-9 <NAG>
 A:Cross-references: GB:S73265; NID:9685049; PIDN:AA14116.1; PID:94261816
 R:Lebacqz-Verheyden, A.M.; Kasprzyk, P.G.; Raum, M.G.; Van Wyke Coelinh, K.; Lebacqz, J.A
 Mol. Cell. Biol. 8, 3129-3135, 1988
 A:Title: Posttranslational processing of endogenous and of baculovirus-expressed human g
 A:Reference number: A31200; MUID:89096899
 A:Contents: annotation
 C:Comment: The nomenclature for the precursor splice forms I, II, and III is taken from
 C:Genetics:
 A:Gene: GDB:GRP
 A:Cross-references: GDB:119284; OMIM:137260
 A:Map position: 18q21.32-18q21.33
 C:Superfamily: gastrin-releasing peptide
 C:Keywords: alternative splicing; amidated carboxyl end; neuropeptide
 F:1-148/Product: gastrin-releasing peptide precursor splice form I #status predicted <SF
 F:1-127,135-148/Product: gastrin-releasing peptide precursor splice form II #status pred
 F:1-123/Domains: signal sequence #status predicted <SIG>
 F:24-50/Product: gastrin-releasing peptide #status experimental <MAT1>
 F:41-50/Product: neuromedin C #status experimental <MAT2>
 F:50/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 17.28; Score 97.5; DB 1; Length 148;
 Best Local Similarity 34.58; Pred. No. 0.0042;
 Matches 40; Conservative 13; Mismatches 26; Indels 37; Gaps 7;
 QY 1 MFGSLHFAALLAAGVPLSMPLPPRSASKI-----RVHSRGLMAIGHFMGKKS 51
 Db 1 MRGSELPLVLLAL-VLCIA-----PRGRAVPLPAGGGVTLMKMPRGHMAVGHLMGKKS 54
 QY 52 L-EPPSSPPLGTAPHTSLRDQRL-----QLSHDLGLILLK-----KALG 90
 Db 55 TGESSSVSERS-----SLKQQLREVIRMEEARNLGLIEAKENRNHQPQPKALG 105

RESULT 6
 147010
 gastrin-releasing peptide - sheep
 C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)
 C:Date: 15-Oct-1996 #sequence, revision 15-Oct-1996 #text, change 19-Jan-2001
 C:Accession: 147010
 R:Fraser, M.; McDonald, T.J.; Spindel, E.R.; Fahy, M.; Hall, D.; Challis, J.R.
 Endocrinology 135, 2440-2445, 1994
 A:Title: Gastrin-releasing peptide is produced in the pregnant ovine uterus.
 A:Reference number: 147010; MUID:95080110
 A:Accession: 147010
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-134 <FRA>
 A:Cross-references: GB:S75723; NID:9913167; PIDN:AA32675.1; PID:9913168
 C:Superfamily: gastrin-releasing peptide

Query Match 16.88; Score 95.5; DB 2; Length 134;
 Best Local Similarity 29.88; Pred. No. 0.0061;

Matches 28; Conservative 17; Mismatches 30; Indels 19; Gaps 3;
 QY 23 PEPRSASKI-----RVHSRGLMAIGHFMGKKSLEPSSPLGTAPHTSLRD-Q 71
 Db 17 PAPGSAAPVYAGAGALAKATKMYTGRGNHMAVGHLMGKKSVAESPQLREESLEQLREYAQ 76
 QY 72 RLQSLHDLGLILLKALG-----VSLSRPA 97
 Db 77 WEATRNLSILQAKVAQGHOPPMPEPLSTQPA 110

RESULT 7
 A47201
 bombesinlike peptide - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 21-Sep-1993 #sequence, revision 18-Nov-1994 #text, change 04-Sep-1998
 C:Accession: A47201
 R:Weschelberger, C.; Kreil, G.; Richter, K.
 Proc. Natl. Acad. Sci. U.S.A. 89, 9819-9822, 1992
 A:Title: Isolation and sequence of a cDNA encoding the precursor of a bombesinlike pe
 A:Reference number: A47201; MUID:93028554
 A:Accession: A47201
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-120 <MEC>
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:115857, NCBI:P:115858)
 C:Superfamily: ranatensin

Query Match 16.58; Score 94; DB 2; Length 120;
 Best Local Similarity 43.68; Pred. No. 0.0077;
 Matches 24; Conservative 6; Mismatches 21; Indels 4; Gaps 2;
 QY 5 LHLFALLAAGVPLSMPLPPRSASKIRVHSRGLMAIGHFMGKKSLEPS 58
 Db 15 LTHLLSLFPLVLCMEFSEEDARNIEKIR--RGNQVAGHFMGKKSLODTNPS 66

RESULT 8
 A40922
 gastrin-releasing peptide precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 06-Mar-1992 #sequence, revision 06-Mar-1992 #text, change 16-Jul-1999
 C:Accession: A40922
 R:Lebacqz-Verheyden, A.M.; Krystal, G.; Sartor, O.; Way, J.; Batley, J.F.
 Mol. Endocrinol. 2, 556-563, 1988
 A:Title: The rat prepro gastrin releasing peptide gene is transcribed from two initia
 A:Reference number: A40922; MUID:8834558
 A:Accession: A40922
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-147 <LEB>
 A:Cross-references: GB:M31176; NID:9204256; PIDN:AAA41197.1; PID:9204257
 C:Superfamily: gastrin-releasing peptide
 C:Keywords: neuropeptide

Query Match 15.98; Score 90.5; DB 2; Length 147;
 Best Local Similarity 28.88; Pred. No. 0.023;
 Matches 34; Conservative 16; Mismatches 39; Indels 29; Gaps 5;
 QY 1 MFGSLHFAALLAAGVPLSMPLPPRSASKI-----RVHSRGLMAIGHFMGK 49
 Db 1 MRGSELPLVLLALV-----CQAPRGPAVSTGAGGVTLMKMPRGSHMAVGHLMGK 54
 QY 50 KLEPSSPPLGTAPHTSLRDQRL-----QLSHDLGLILLKRALGVSLSRPAPO 101
 Db 55 KSTD-ELPPIYAADRDLKQLNGYIRMEEARNLGLILEASR-----NRSHQPPQ 106

RESULT 9
 A42437

gastrin-releasing peptide - Bombina orientalis
 C:Species: Bombina orientalis
 C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
 C:Accession: A42437
 R:Nagalla, S.R.; Gibson, B.W.; Tang, D.; Reeve Jr., J.R.; Spindel, E.R.
 J. Biol. Chem. 267, 6916-6922, 1992
 A:Title: Gastrin-releasing peptide (GRP) is not mammalian bombesin. Identification and
 A:Reference number: A42437; MUID:92202250
 A:Accession: A42437
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-155 <NAG>
 A:Cross-references: GB:M83737; MID:g211018; PIDN:AAA51409.1; PID:g211019
 A>Note: sequence extracted from NCBI backbone (NCBIN:91643; NCBIPI:91645)
 C:Superfamily: gastrin-releasing peptide
 C:Keywords: neuropeptide

Query Match 14.6%; Score 83; DB 2; Length 155;
 Best Local Similarity 40.7%; Pred. No. 0.15;
 Matches 22; Conservative 8; Mismatches 18; Indels 6; Gaps 2;

QY 6 LHFALLAGV---VPLSMDLP---EPRSRASKIRVHSGKLMAGHFMGKKSLE 53
 DB 13 LFFLVLCSLVLCCKVHLSQASPTSQOHNDASLSKIPKSGHMAVGHLMGKKSIE 66

RESULT 10
 B57058

Phc-8 phyliolitorin precursor - Sauvage's leaf frog
 C:Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
 C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 24-Sep-1999
 C:Accession: B57058
 R:Nagalla, S.R.; Barry, B.J.; Spindel, E.R.
 Mol. Endocrinol. 8, 943-951, 1994
 A:Title: Cloning of complementary DNAs encoding the amphibian bombesin-like peptides Phc
 ropeptide diversity.
 A:Reference number: A57058; MUID:95089778
 A:Accession: B57058
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-90 <NAG>
 A:Cross-references: GB:S77226; MID:g998449; PIDN:AAH32788.1; PID:g998450
 C:Superfamily: ranatensin

Query Match 14.0%; Score 79.5; DB 2; Length 90;
 Best Local Similarity 41.2%; Pred. No. 0.19;
 Matches 21; Conservative 6; Mismatches 23; Indels 1; Gaps 1;

QY 3 GSLHFAALLAGVPLSMDLPEPRSRASKIRVHSGKLMAGHFMGKKSLE 53
 DB 14 GFLAHLLSTFVLTVCYKEVTEESDDLKSRNVLQR-QLMAVGSFMGKKSLE 63

RESULT 11
 A39261

bombesin precursor - Bombina orientalis
 C:Species: Bombina orientalis
 C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 24-Sep-1999
 C:Accession: A39261
 R:Spindel, E.R.; Gibson, B.W.; Reeve Jr., J.R.; Kelly, M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 9813-9817, 1990
 A:Title: Cloning of cDNAs encoding amphibian bombesin: evidence for the relationship bet
 A:Reference number: A39261; MUID:91088602
 A:Accession: A39261
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-119 <SPI>
 A:Cross-references: GB:M55255; MID:g211016; PIDN:AAA48551.1; PID:g211017
 C:Superfamily: ranatensin
 C:Keywords: neuropeptide

Query Match 13.6%; Score 77.5; DB 2; Length 119;
 Best Local Similarity 30.3%; Pred. No. 0.43;
 Matches 23; Conservative 13; Mismatches 35; Indels 5; Gaps 3;

QY 3 GSLHFAALLAGVPLS---WDLPEPRSRASKIRVHSGKLMAGHFMGKKSLEPSSPSP 59
 DB 13 GFLFH--LIFSFISLSSCMFEVEDPNNQGRISLQQRIGNOMAVGHLMGKKSLEDDTDFEE 70

QY 60 LGTAHPTSLRQORLOL 75
 DB 71 MESFAKRNVENRRAL 86

RESULT 12
 A34203

DNA-binding protein PRDII-BF1 - human
 N:Alternate names: major histocompatibility complex enhancer-binding protein 1
 C:Species: Homo sapiens (man)
 C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
 C:Accession: A34203; A34779
 R:Fan, C.M.; Maniatis, T.
 Genes Dev. 4, 29-42, 1990
 A:Title: A DNA-binding protein containing two widely separated zinc finger motifs tha
 A:Reference number: A34203; MUID:90169514
 A:Accession: A34203
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2717 <FAN>
 A:Cross-references: EMBL:X51435; MID:g38017; PIDN:CA35798.1; PID:g38018
 R:Baladin Jr., A.S.; LeClair, K.P.; Singh, H.; Sharp, P.A.
 Mol. Cell. Biol. 10, 1406-1414, 1990
 A:Title: A large protein containing zinc finger domains binds to related sequence ele
 A:Reference number: A34779; MUID:90205817
 A:Accession: A34779
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 801-1072, 'N', 1074-1168, 'K', 1170-1225, 'V', 1227-1434, 'N', 1436-1607, 'I', 1609
 A:Cross-references: GB:M32019
 C:Superfamily: HIV-EP2 enhancer-binding protein
 C:Keywords: DNA binding; transcription regulation; zinc finger

Query Match 13.1%; Score 74.5; DB 2; Length 2717;
 Best Local Similarity 38.4%; Pred. No. 38;
 Matches 28; Conservative 5; Mismatches 23; Indels 17; Gaps 3;

QY 17 PLSMDLPEPRSRASKI-----RVHSGKLMAGHFMGKKSLEPSSPPLGTAHPTSLRD 70
 DB 1144 PMSFKPEPPERASPVSFQELNRTGNSGLKYIG-----ISOESHPSKDSHPH----- 1193

QY 71 ORLOLSDHLDLGL 83
 DB 1194 -QLALSDALRGEL 1205

RESULT 13
 A36949

28.9K basic DNA-binding protein - Mycobacterium scrofulaceum plasmid pMSC262
 C:Species: Mycobacterium scrofulaceum
 C:Date: 06-Oct-1994 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997
 C:Accession: A36949
 R:Qin, M.; Taniguchi, H.; Mizuguchi, Y.
 J. Bacteriol. 176, 419-425, 1994
 A:Title: Analysis of the replication region of a mycobacterial plasmid, pMSC262.
 A:Reference number: A36949; MUID:94117377
 A:Accession: A36949
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-260 <QIN>
 A>Note: sequence extracted from NCBI backbone (NCBIN:142814, NCBIPI:142815)
 C:Genetics:
 A:Genome: plasmid

Query Match	13.0%	Score 74;	DB 2;	length 260;
Best Local Similarity	27.6%;	Pred. NO. 2.6;		
Matches 27;	Conservative 16;	Mismatches 45;	Indels 10;	Gaps 4;

OY 14 GVVPLSWDLP---EPRSRASKLRVHSRCKLMAIGHFMGKSKLEPSSP-SPLGTAPHITSLR 69
 ||:::|||::|||::|::|::|::|::|:
Db 71 GVIGTAGTGPEDRRQQRSAADRYTRHHRHRLRVVAAVIIGHENRPSPPLKPGGPYTRHRTIR 130

```

QY 70 DQRLQSHD-----LGITLLKKAALGVSLSRPAQIQY 102
      :|:      |||:  |  |||:  ;
Db 131 G-LAELEHNRRDSRLGSLAVLMLGGRRPRPRPTH 167

```

Citation	Accession	Date	Author
Integral membrane protein [imported] - Caulobacter crescentus		30-Nov-2001	Watanabe et al.
C;Species: Caulobacter crescentus		30-Nov-2001	Watanabe et al.
C;Date: 30-Nov-2001	Accession	30-Nov-2001	Watanabe et al.

C;Accession: F87567
R.Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.C.; Debby, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonin, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. *Proc. Natl. Acad. Sci. U.S.A.* 98, 4136-4141, 2001

A;Title:Complete Genome Sequence of *Caulobacter crescentus*
A;Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: F8/56/

A;Status: preliminary

A;Residues: 1-297 <STO>
A;molecule type: DNA

A; Cross-references: GB:AE005673; NID:g13424136; PIDN:AAK24538.1; GSPDB:GN00148

C;Genetics:
A;Gene: CC2568

Query Match	13.0%; Score 74; DB 2; Length 297;
-------------	------------------------------------

Best Local Similarity 29.0%; Pred. No. 3.1;
Matches 31; Conservative 20; Mismatches 26; Indels 30; Gaps 77

QY 1 MFGSLHFAALLAGVVPSPWDLPEPRSRASKIRVHSGKLMIAIGH----FMGKKLEPSS 566
 :::::||||:|||||:||||:||||:
 Db 35 LYAAVRFALVAALTLF--WLLPAPRPRTWVLY---GLIMGCGNFALLFMGFQNASPSA 899

```
QY      57 PS---PLGTRPHTSLRDQRQLSHDLGLLL-----KKALGVSL 94
          | :| |:| :||::|:|
Db     90 ASVVIQGV-VPTT-----LSSLILGEKIRWRRGSLALT 124
```

G82806
 DNA primase XF0430 [imported] - *Xylella fastidiosa* (strain 9a5c)

C:species: *xyliella fastidiosa*
C:date: 18-Aug-2000 #sequence: 20-Aug-2000 #text_change: 14-Dec-2000

C;Accession: G82806
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences

Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*

A;Reference number: A82515; MUID:20365717

A/Note: For a complete list of authors see reference number A59328 below
A/Accession: G82806

A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-577 <SIM>

A:cross-references: GR:AE003894; GB:AE003849; NID:910526//; PIDN:AMF83240.1; GSPDB:GN00

R; Simpson, A. J. G.; Reimach, F. C.;

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. *Biomed. Res.* 2000, 11, 113-117.

Submitted to GenBank, June 2000

J.D.: Junqueira, M.L.; Kemper, E.L.; Krieger, J.E.; Kuramae, E.E.; Laigys

Chadot, M.A.; Medeira, A.M.B.N.; Medeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Mirecca, E.C.; Miyaki, C.C.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.U. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawaia, R.A.;
A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A;Gene: XF0430
C;Superfamily: DNA primase

Query Match	13.08	Score 74	DB 2	Length 577
Best Local Similarity	27.88	Pred. No. 6.8		
Matches 27	Conservative 12	Mismatches 36	Indels 22	Gaps 4

```

QY      9 ALLAGVPLTSMDLPE-----PSRSASIRVHSRGKLAIGHFMKKSLSSPSPLGT 62
          |||  ||  |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     385 ARLEERAPLIMKIPEGAFNDIMQR-----LAHLGVNIADH-GPAPAT 429

```

QY 63 A-PHTSLRDQRLQSLHDLGLILLKALGVSLSRAP 98
:| | | :| | :| | :| | :| |
Db 430 SRPATRLPAQKRNLHTTIALITLQPSLAWMTNTPYP 466

Search completed: May 30, 2002, 17:25:17
Job time: 122 sec

Job time: 122 sec

